

MODELING AND SIMULATION OF SHRIMP DISEASES PROPAGATION IN RIVER NETWORKS AND INSIDE POND

TUYEN T. T. TRUONG, HIEP X. HUYNH, AND ALEXIS DROGOUL

ABSTRACT

In this paper we study and apply modeling on agent-based simulation for simulating the mechanism of shrimp infection inside shrimp-ponds and on the river networks in the region of Mekong Delta, Vietnam. The disease-propagation rules were established based on the way that the pathogens multiply in water-flows together with other infecting agents such as aquatic or migrating living things. Inside a shrimp-pond, besides the factors mentioned above, the infecting mechanism also depends on the density of shrimps and the initial number of the pathogens. In this study, we constructed two on-river-infecting scenarios for cases of the occurrence or non-occurrence of the pathogens and two inside one shrimp-pond infecting scenarios. All of the results are written in GAML and executed on GAMA platform.

Keywords. modeling, agent-based simulation, mechanism of disease-propagation, GAMA platform.

1. INTRODUCTION

With good geographical location and natural conditions, shrimp hatching in Mekong Delta are grown rapidly and provides a lot of sea-products in Vietnam as well as in foreign countries. Besides the increase in farming area, the growing level of shrimps' diseases is also spread quickly based on the polluted water, flow of water and healthy status of shrimps.

According to the aquaculture experts, there is no treatment to cure the shrimp-diseases caused by virus especially White Spot Syndrome Virus (WSSV) [3, 8, 9]. As a result, farmers need to protect their shrimps and prevent propagation of diseases from ponds to ponds and inside shrimp pond as well [5].

The propagation of shrimp-diseases based on many features such as flow and speed of water in the rivers, salt level, pH level, high level of water, the status of pond, the movement of birds, crabs, snakes, status of shrimps, using chemical or not.... Because of these complicated factors, nowadays, there is no model of shrimp disease propagation either in Vietnam or in the world. In fact, there is an article about propagation of H5N1 virus in north Vietnam [2], which treat the same topic. This article also models the propagation of disease in Vietnam but is based on social structure and animal' behavior. In our model, the rules are established in mathematical formulae.

This paper presents WSSV propagation models in both large scale (in river networks) and small scale (inside one shrimp-pond). It also introduces the simulation tool and some scenarios in experimentation. The main purpose of our work is modeling and simulating the shrimp-disease (especially WSSV) propagation with specific input data and then the results hopefully support making decision.

The structure of this paper includes five parts. The first part is an introduction which briefly shows the motivation of this paper and some related work. Models will be presented in the second part. The next one is simulation part. In this part, we describe about how to simulate the propagation models. Another part is experimentation part, which shows some scenarios and evaluate the results. The last part is conclusion.

2. SHRIMP DISEASE PROPAGATION MODEL

The mechanism of WSSV propagation in river networks and inside one shrimp-pond are different, so it is separated into two small models: propagation in the river networks and propagation inside shrimp-pond. These two models influence each other. With specific of environment, WSSVs propagate along the rivers and they can move into ponds through drains (the doors of ponds) or the movement of the animals such as birds, snakes, crabs, mice, fish, etc.... Besides, inside shrimp-pond, WSSVs multiply based on the real condition of environment in this pond as well as characteristics of shrimps such as health status, density of shrimp, and chemical, etc.... The general model of WSSV propagation is presented as figure 1.

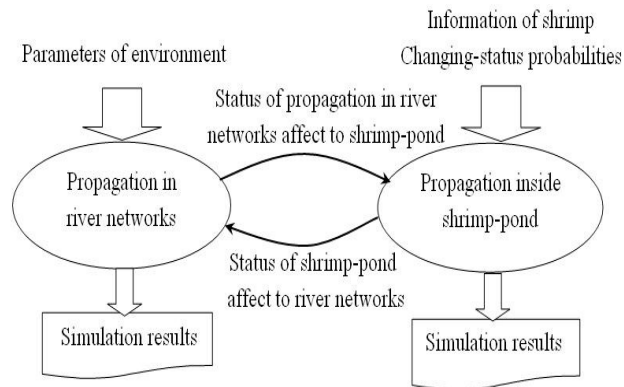


Figure 1. The general model of WSSV propagation

2.1. Propagation of WSSV in river networks Model

The WSSV are existent in water and move with the flow of water in river networks. They can exist about 4-5 days in the river networks with common conditions of temperature, salt level, pH level [5, 11]. There are two ways WSSV propagate in river networks. The first way is through the flow of water in the rivers and the other way is the movement of birds, crabs, snakes, mice and fish, etc.... from infected areas to other areas. In the first way, the direction of water current is named from 0 to 7 as shown in figure 2. Besides, the tide on river networks changes

every 6 and a quarter hours, so the formula to calculate the direction of river's current is presented in (1)

$$watercurrent(k) = (watercurrent(k - 1) + 4) \bmod 8. \quad (1)$$

The transfer of water in river from cell to cell depends on the direction of water in river. We establish the rule for the transfer of water in river networks as (3). Water will be sent 50% to next cell (updating-cell) if sending-cell is in main direction and 25% will be sent for 2 secondary directions. The old water of updating-cell is also transmitted to next cells (receiving-cells) in the same way. We name seven neighbor cells of updating-cell from VT1 to VT7 based on the direction of water.

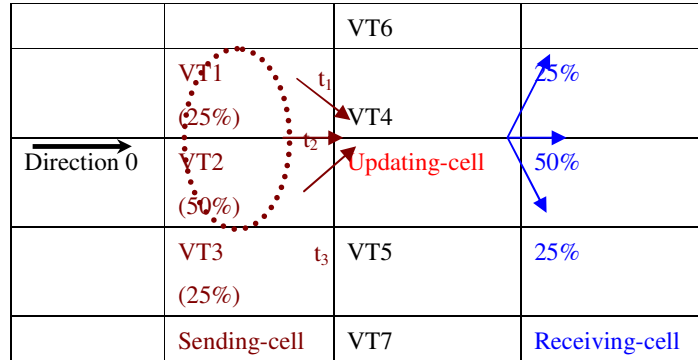
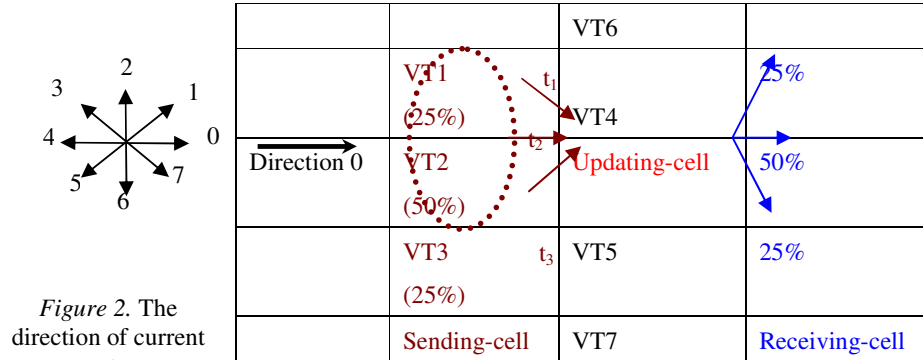
In this scale, the neighbors of updating-cell which must check for picking up the percentages in updating information of water in river are stored in constant dimensions:

$$Differ = \begin{pmatrix} -1, & 0, & -1, & 0, & 1, & 1, & -1, & 0, & -1, & -1, & -1, & -1, & 0, & 1, & 1 \\ -1, & -1, & 0, & 1, & 1, & 1, & 0, & -1, & 0, & -1, & -1, & -1, & 0, & 1, & 1 \\ -1, & -1, & 1, & 1, & 1, & 0, & 1, & -1, & 1, & 0, & -1, & 0, & 1, & 1, & 0 \\ 0, & 1, & -1, & -1, & 0, & 0, & -1, & 1, & -1, & 0, & 0, & 0, & -1, & -1, & 0, & 0 \\ 0, & 0, & 1, & 0, & 0, & -1, & 1, & 0, & 1, & 1, & 0, & 1, & 1, & 0, & 0, & -1 \\ 0, & -1, & -2, & -1, & 0, & -1, & 1, & 0, & -2, & -1, & 1, & 1, & 1, & 0, & 0, & -1 \\ 0, & -1, & 2, & 1, & 0, & -1, & 1, & 0, & 2, & 2, & 0, & -1, & 1, & 0, & 0, & -1 \end{pmatrix}$$

Then, the formula to define the location of 7 neighbor cells is shown in (2)

$$\begin{aligned} x_{VTi} &= x_{updatingcell} + Differ[i, watercurrent] \\ y_{VTi} &= y_{updatingcell} + Differ[i, 8 + watercurrent] \end{aligned} \quad (2)$$

For example, the water will be calculated with direction 0 as figure 3. In this direction, the updating-cell will be received 50% water from VT2, 25 water % from VT1 and 25% water from VT3. Moreover, The old water in updating-cell also move to receiving-cells with scale :25%, 50% and 25%.



In addition, these percentages can be changed based on whether received-cells are water-cell or not. For example, in direction 0 (see figure 3), the transfer percentages are based on neighbor cells: VT4, VT6, VT5, VT7 being water cells or not.

Following the first rule, the transfer percentages are presented in (3)

$$t_1 = \begin{cases} 0 & \text{If VT1 is not a water-cell} \\ 25\% * gt(VT1) & \text{If VT1, VT4 and VT6 are water-cells} \\ 50\% * gt(VT1) & \text{If VT4 nor VT6 is not a water-cell} \\ 75\% * gt(VT1) & \text{If both VT4 and VT6 are not water-cells} \end{cases} \quad (3)$$

$$t_2 = \begin{cases} 0 & \text{If VT2 is not a water-cell} \\ 50\% * gt(VT2) & \text{If VT2, VT4 and VT5 are water-cells} \\ 75\% * gt(VT2) & \text{If VT4 nor VT5 is not a water-cell} \\ 100\% * gt(VT2) & \text{If both VT4 and VT5 are not water-cells} \end{cases}$$

$$t_3 = \begin{cases} 0 & \text{If VT3 is not a water-cell} \\ 25\% * gt(VT3) & \text{If VT3, VT5 and VT7 are water-cells} \\ 50\% * gt(VT3) & \text{If VT5 nor VT7 is not a water-cell} \\ 0.75 * gt(VT3) & \text{If both VT5 and VT7 are not water-cells} \end{cases}$$

The formula (3) presents the amount of sending-water from three main sending-cells (VT1, VT2,VT3) to updating-cell. The information of water is stored in $gt(VT_i)$.

The location of these neighbor cells depend on the direction of water current in river networks and the location of updating-cell. This paper determines the formula to calculate the water in updating-cell (4).

$$N_{i,j}(t) = \{t_1 + t_2 + t_3\} * sent_rate + N_{i,j}(t-1) * \{1 - sent_rate\} \quad (4)$$

In the formula (4), t_1, t_2, t_3 are determined in (3) and $sent_rate$ is a variable which shows the average transfer-rate of water in river networks.

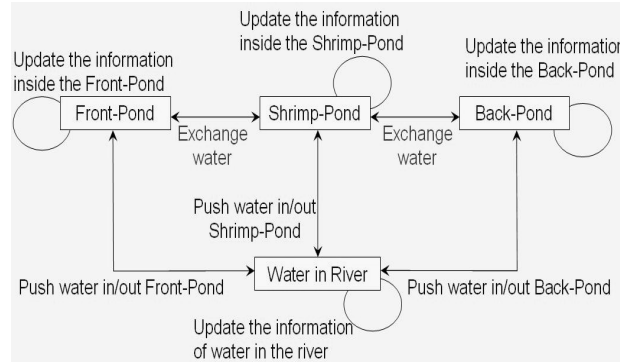


Figure 4. WSSV Propagation in river networks model

The second rule is the death-rate of WSSV. The life-time of WSSV in water depend on the temperature, pH level, salt level of water [9]. Therefore, the death-rate of WSSV is constructed as a function $f(x, y, z)$ with three parameters: temperature, pH level and salt level.

The last rule is the rule about inlet/outlet water to ponds. The pond can receive new water or not based on the difference of high level of water inside and outside the pond, the status of drain (closed or opened) and whether pond is linked to front-pond, back-pond or not.

With three rules above, the model of WSSV propagation in river networks is shown in figure 4. There are three types of pond: Front-pond, Shrimp-pond and Back-Pond. The front-pond is the pond which process water before transmitting to shrimp-pond. The back-pond is the pond which process water before returning to river networks. Shrimp-pond is the pond in which shrimps are fed. Information of water in river and water inside ponds are updated as two first rules above. The exchange water inside and outside pond follow the last rule.

2.2. Propagation of WSSV Model inside one Shrimp-Pond

The mechanism infection of WSSVs and infected-shrimps inside one shrimp-pond is dependent on the contact between shrimps with WSSVs, infected-shrimps with healthy-shrimps and the level of temperature, salt, pH of water [1,3, 4, 15]. The WSSV propagation inside one shrimp-pond model is built as figure 5. There are three objects in this model: Shrimp-pond, Shrimp and Pathogen. The information of water inside shrimp-pond is updated because of changing water, evaporating water, rain falling. Shrimps move randomly inside shrimp-pond only and they can be died. Death-shrimps can release pathogens in water. These pathogens directly infect other shrimps, so shrimps can change their health status.

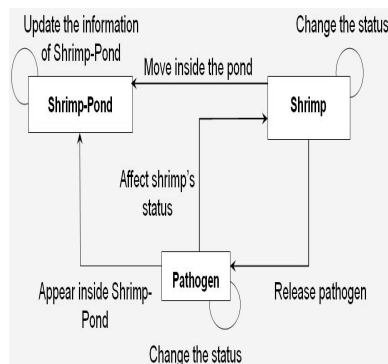


Figure 5. WSSV Propagation inside one shrimp-pond Model

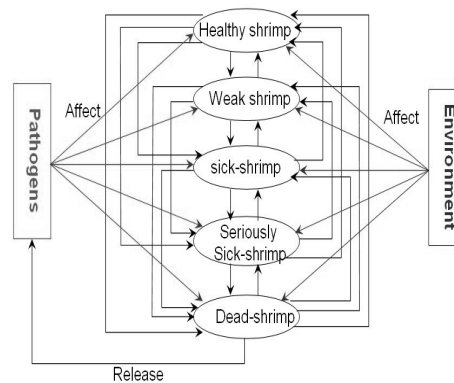


Figure 6. The changing status mechanism

The changing status of shrimp from healthy shrimp to seriously infected shrimp are based on the current status of shrimp and the changing probabilities as shown in figure 6. These probabilities are stored in matrix and we calculate the number of shrimps in each status by Markov chain. For example, at the current time, the number of shrimps in each status are (100, 20, 10, 0, 0), after 1 step (15 minus) in the environment with pathogens, they can be (99, 20, 9, 1, 0). These results are also based on the number of pathogens inside water and the movement of shrimps whether they are within an infected-radius or not. And then, those results will be changed for next step, and next step...

3. SHRIMP DISEASE PROPAGATION SIMULATION

We simulate the WSSV propagation in GAMA platform. Our simulation tool is divided into three packages. The first package is simulation in river networks, the second one is simulation inside one shrimp-pond and the last is connectivity package which links two other packages together as shown in figure 7.

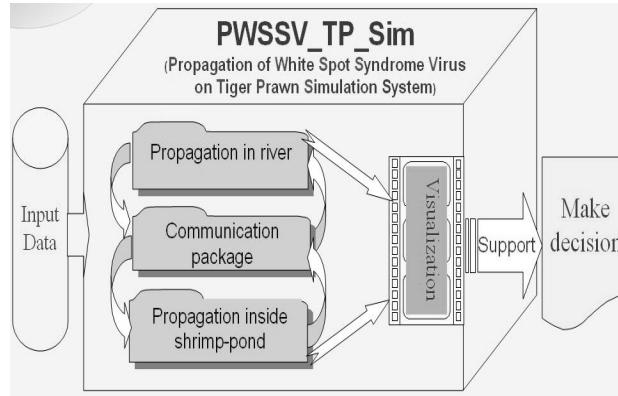


Figure 7. The structure of simulation tool

The parameters of the model are information of water in river, starting simulation time, the number of simulation-days, information of WSSV in river, information on shrimps and the way to solve the disease in figure 8. The simulation process is presented in figure 9. Firstly, the model will get input data and then load the map and initialize the simulation environment. After having simulation environment, the updating information of water in river and inside shrimp-pond will be executed step by step until reaching the end of simulation day.

Figure 8. The parameters of the model

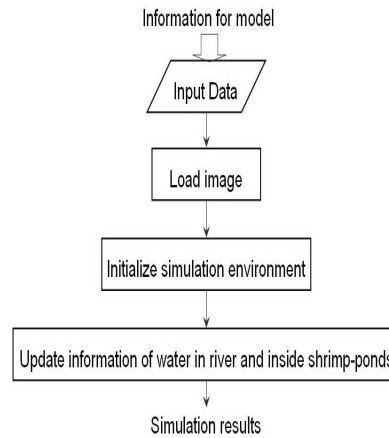


Figure 9. The simulation process

3.1. Simulation of WSSV Propagation in river networks

We simulated the propagation of WSSV in SocTrang province with real river networks. The simulation environment is built by an image in grid with size 200×200 . Each cell represents 0.45 km^2 in real environment. We built a map of SocTrang Province with river networks, and set up shrimp-ponds (with and without Front-Pond, Back-Pond) along the river networks and other components such as: province boulder, district boulder, road networks, etc....

In large scale, there are four agents such as: shrimp-pond, front-pond, back-pond, water. The behavior of ponds are characterized by open/close the drains, update information inside the ponds for water inlet/outlet the ponds. The behaviors of water in the rivers are update the in formation of water in rivers based on the flow of water in rivers, push water in/out ponds, the death-rate of WSSV and the appearance of WSSV based on the migrating living things.

In this scale, the main behavior is updating information of water in river. The neighbors of updating-cell which must check for picking up the percentages in updating information of water in river are stored in constant dimensions and the neighbor cells are defined in (2) and the formula to update information of water in (4). As a result, the updating information action is presented in figure 10.

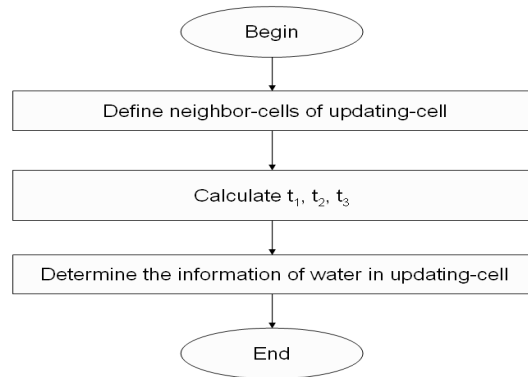








Figure 10. Describe action update_information_water in river networks

The results will be presented by different color. The infection status of the shrimp-ponds are shown in different colors as table 1.

Table 1. The colors which present the infected status of shrimp-pond

Color	RGB	Explanation
	[200, 255, 200]	Healthy shrimp-pond
	[255, 0, 0]	Susceptible shrimp-pond
	[0, 10, 200]	Infected shrimp-pond
	[124, 20, 20]	Seriously infected shrimp-pond
	[128, 255, 255]	Front-pond
	[190, 200, 220]	Back-pond

3.2. Simulation of WSSV Propagation inside one shrimp-pond

In this small scale, there are three agents: shrimp, pathogen and shrimp-pond. Shrimp can move randomly, change status based on changing probabilities and release pathogens when it die. The pathogen can move and die based on the environment's conditions as well as presence of chemicals or not in this pond. Shrimp-pond can open/close the drain to exchange water and update the information of water inside shrimp-pond.

Each behavior will be simulated by an action in GAMA. For example, the action changing healthy status of shrimp is described in figure 11.

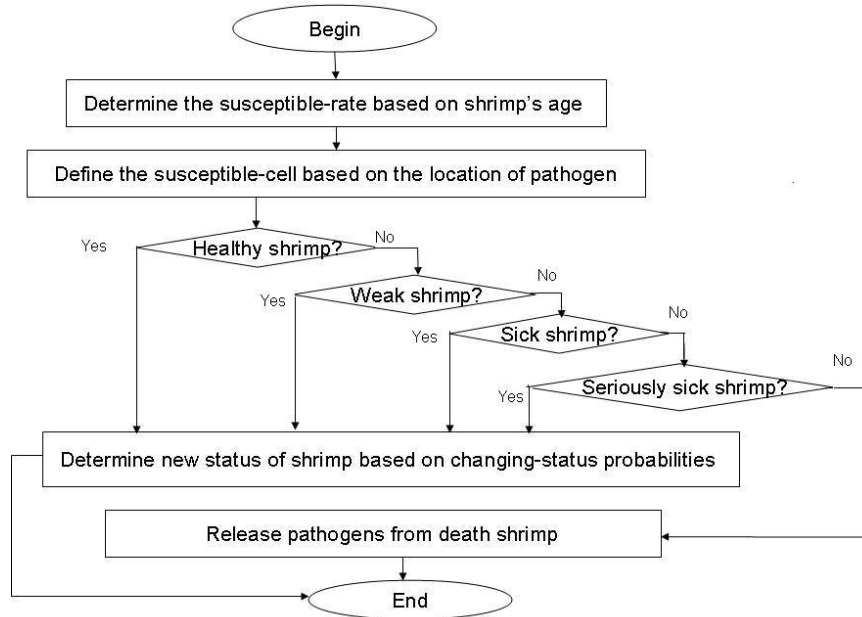


Figure 11. Describe the action changing status

4. EXPERIMENTATION

We construct 2 main simulation scenarios for large scale (figure 12) and small scale (figure 13). In propagation in river networks, we simulate with different input data such as the initial appeared location of WSSV in river networks, the number of WSSVs in each location and the information of environment: temperature, pH level, salt level of water, time to start to simulate,...etc. In general, the experimental results show that: the number of infected shrimp-ponds without front-pond is always much more greater than infected shrimp-ponds with front-pond; In addition, infected ponds are usually the opened-drain ponds to exchange water; It also presents the appearance of WSSV randomly in the river networks because of the movement of birds, crabs, snakes, etc... These results show the agreement with warning of hydrology experts.



Figure 12. The initial simulation in river networks

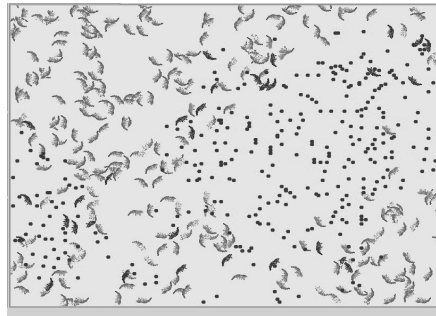


Figure 13. The simulation result inside shrimp-pond

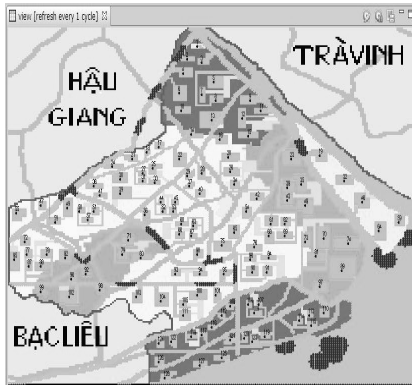


Figure 14. Pathogens appear in river networks at the initial time

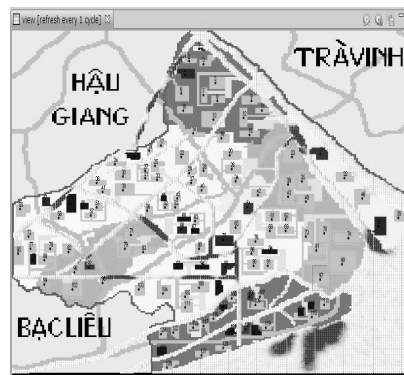


Figure 15. The simulation result after 5 days

For example, if there are 15 locations at which WSSVs appeared (figure 14) at the initial simulation time, after 5 days, the WSSVs will propagate as in figure 15. At that time, the numbers of infected shrimp-pond is 11 ponds while number of shrimp-pond with front-pond is 2 (18.2%).

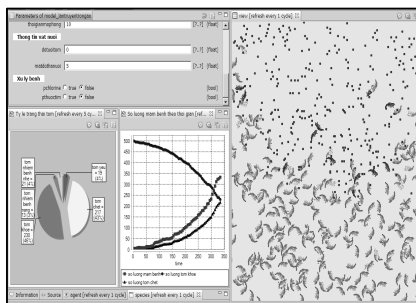


Figure 16. Having pathogens inside shrimp-pond

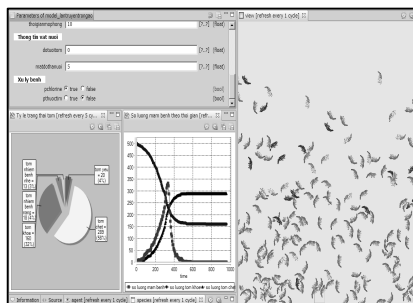


Figure 17. Using chemical to solve the disease

In small scale, we also change the input data to show the effects of environment, time, chemical to harvest. The experimentation shows that using or not chemicals and when to use them will influence the harvests very much as shown in figures 16, 17. The chemical is not a cure for infected shrimps but it can kill the WSSVs in water. We also keep chemicals in water about 7 days and after that the chemicals effect dies out. As a result, if farmers use chemicals too early, it would be not helpful. Moreover, the density of shrimp also affects the propagation. The higher density of shrimp, the faster WSSVs multiply inside one shrimp-pond. The starting time and the age of postlarvae are also important because of the difference of weather at that time. The GAP standard suggests that, the density of shrimp should be 5 - 7 postlarvae/m² and the starting time for harvest from the end of February to March [1].

5. CONCLUSIONS

The paper shows the model and simulation tool about the WSSV propagation both in river networks and inside one shrimp-pond. We established the disease propagation rules in river network and inside one shrimp-pond. All rules are presented in mathematical formulae to make it easy to program. This paper shows two models: Disease propagation in river network and WSSV diffusion inside one shrimp-pond which affected each other. The PWSSV_TP_Sim tool is constructed in GAMA platform with 3 packages and more than 1200 lines of code. Besides, two main scenarios is built: propagation in river networks and propagation inside shrimp-pond, to evaluate the simulation results.

In summary, the application of technical modeling and multi agent-based simulation (MABS) technology not only fulfill the objectives about modeling and simulating the mechanisms for propagation of WSSV in tiger shrimps, it also shows the positive outlook in developing applications by MABS.

In this paper, all probabilities in our model are based on the knowledge of aquacultural experts and are kept as constants. The model can further develop if these probabilities can be changed based on the real environment and history data. In fact, we can determine the probabilities in model by intelligent algorithms such as decision tree and Bayesian network to adjust the probabilities in specific environment.

In this paper, the simulation results present the mechanism of spread of disease on shrimp, but in our model exists a weakness: the probabilities which are used in our model, are based on the knowledge of aquacultural experts and are kept as constants. Indeed, these probabilities may change depending on factors such as flow water's speed, type of postlarvae, density of shrimp, infection radius of WSSV, shrimp's status, etc... Therefore, to improve the model, these probabilities should be determined by using some intelligent algorithms such as decision trees, Bayesian networks to match the specific environment during the simulation. Estimating these probabilities is completely feasible if mining is done on actual data which are provided by the extension center in the Mekong Delta.

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Address:

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Tuyen T. T. Truong, Hiep X. Huynh,

College of Information Technology, Can Tho University, Vietnam.

Alexis Drogoul,

Umi 209 Ummisco, Ird/Upmc, France.

